Cancelled per pt. 18/c

SEQUENCE LISTING

<110> PARANHOS-BACCALA, Glaucia

KOMURIAN-PRADEL, Florence

BEDIN, Frederic

SODOYER, Mireille

OTT, Catherine

MALLET, Francois

PERRON, Herve

MANDRAND, Bernard

<120> RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR, ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES

<130> 103514

<140> US/09/319,156

<141> 1999-11-02

<150> PCT/FR98/01460

<151> 1998-07-07

<150> FR/97/08816

<151> 1997-07-07

<160> 45

<170> PatentIn version 3.0

<210> 1

<211> 34

<212> DNA

<213> MSRV

<400> 1

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<210> 2

<211> 30

<212> DNA

<213> MSRV

<400> 2

gccatcaagc cacccaagaa ctcttaactt 30

<210> 3

<211> 30

<212> DNA

<213> MSRV

<400> 3

ccaatagcca gaccattata tacactaatt 30

<210> 4

<211> 310

<212> DNA

<213> MSRV

<400> 4

gcttatagaa ggacccctag tatggggtaa tcccctctgg gaaaccaagc cccagtactc 60

agcaggaaaa atagaatagg aaacctcaca aggacatact ttcctcccct ccagatggct 120

agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac 180

ccttcaccaa accttccact taggcattga tagcacccat cagatggcca aattattatt 240

tactggacca ggccttttca aaactatcaa gaagatagtc aggggctgtg aagtgtgcca 300

aagaaataat 310

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<211> 103

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<213> MSRV

<220>

<221> misc_feature

<222> (26)..(26)

<223> Xaa = any amino acid

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1 5 10 15

Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His
20 25 30

Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
65 70 75 80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys
85 90 95

Glu Val Cys Gln Arg Asn Asn
100

<210> 6

<211> 635

<212> DNA

<213> MSRV

<400> 6

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ctggaccggc ctgctagccc atgctccgat gttaatgaca ttgaaggcac ccctcccgag 180

gaaatctcaa ctgcacaacc cctactatgc cccaattcag cgggaagcag ttagagcggt 240

catcagccaa cctccccaac agcacttggg ttttcctgtt gagaggggggg actgagagac 300

aggactagct ggatttccta ggccaacgaa gaatccctaa gcctagctgg gaaggtgact 360

gcatccacct ctaaacatgg ggcttgcaac ttagctcaca cccgaccaat cagagagctc 420

actaaaatgc taattaggca aaaataggag gtaaagaaat agccaatcat ctattgcctg 480

agagcacagc gggagggaca aggatcggga tataaaccca ggcattcgag ccggcaacgg 540

caacccccctt tgggtcccct ccctttgtat gggcgctctg ttttcactct atttcactct 600

attaaatctt gcaactgaaa aaaaaaaaaa aaaaa 635

<210> 7

<211> 77

<212> PRT

<213> MSRV

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Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile Lys
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Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser
20 25 30

Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
35 40 45

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
50 55 60

Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser
65 70 75

<210> 8

<211> 32

<212> DNA

<213> MSRV

<400> 8
tggggttcca tttgtaagac catctgtagc tt 32

<210> 9

<211> 1481

<212> DNA

<213> MSRV

<400> 9

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acgcggcttc ctggaaatat tgatgcccca tcatatagga gtttatctaa gggaaactcc 180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg 240

catgcaaata ctcattattg gacagggaaa atgattaatc ctagttgtcc tggaggactt 300

ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg gggtggaatt 360

caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat 420

agcaccccta gcccctacaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc 480

catactcgcc tggtgagcct atttaatacc accctcactc ggctccatga ggtctcagcc 540

caaaacccta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc 600

cctgttcctg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta 660

ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt 720

agcaatacta tagacacaac cagctcccaa tgcatcaggt gggtaacacc tcccacacga 780

atagtctgcc taccctcagg aatatttttt gtctgtggta cctcagccta tcattgtttg 840

aatggctctt cagaatctat gtgcttcctc tcattcttag tgcccctat gaccatctac 900

actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtacccatt 960

cttccttttg ttatcagagc aggagtgcta ggcagactag gtactggcat tggcagtatc 1020

acaacctcta ctcagttcta ctacaaacta tctcaagaaa taaatggtga catggaacag 1080

gtcactgact ccctggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt 1140

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ggagaagaac gctgttatta tgttaatcaa tccagaattg tcactgagaa agttaaagaa 1260

attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc 1320

ctcagccaat ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaatattg 1380

ttactcctct ttggaccctg tatctttaac ctccttgtta agtttgtctc ttccagaatt 1440

gaagctgtaa agctacagat ggtcttacaa atggaacccc a 1481

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<211> 493

<212> PRT

<213> MSRV

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<222> (39)..(39)

<223> Xaa = any amino acid

<400> 10

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1               5                  10                  15

Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser
            20                  25                  30

Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
        35                  40                  45

Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
    50                  55                  60

His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
65                  70                  75                  80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
                85                  90                  95

Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
            100                 105                 110

Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
        115                 120                 125
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Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
130 135 140

Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu
180 185 190

His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile
305 310 315 320

Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly
325 330 335

Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
340 345 350

Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu
355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
370 375 380

Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
385 390 395 400

Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
420 425 430

Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val
435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe
450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile
465 470 475 480

Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro
485 490

<210> 11

<211> 32

<212> DNA

<213> MSRV

<400> 11
tcaaaatcga agagctttag acttgctaac cg 32

<210> 12

<211> 1329

<212> DNA

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<222> (1232)..(1232)

<223> n = a, g, c or t/u

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aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct 180

cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt 240

tttactcctc tttggaccct gtatcttcaa cttccttgtt aagtttgtct cttccagaat 300

tgaagctgta aagctacaaa tagttcttca aatggaaccc cagatgcagt ccatgactaa 360

aatctaccgt ggacccctgg accggcctgc tagactatgc tctgatgtta atgacattga 420

agtcacccct cccgaggaaa tctcaactgc acaaccccta ctacactcca attcagtagg 480

aagcagttag agcagttgtc agccaacctc cccaacagta cttgggtttt cctgttgaga 540

gggtggactg agagacagga ctagctggat ttcctaggct gactaagaat cccnaagcct 600

anctgggaag gtgaccgcat ccatctttaa acatggggct tgcaacttag ctcacacccg 660

accaatcaga gagctcacta aaatgctaat caggcaaaaa caggaggtaa agcaatagcc 720

aatcatctat tgcctgagag cacagcggga aggacaagga ttgggatata aactcaggca 780

ttcaagccag caacagcaac ccccttggg tcccctccca ttgtatggga gctctgtttt 840

cactctattt cactctatta aatcatgcaa ctgcactctt ctggtccgtg ttttttatgg 900

ctcaagctga gcttttgttc gccatccacc actgctgttt gccaccgtca cagacccgct 960

gctgacttcc atccctttgg atccagcaga gtgtccactg tgctcctgat ccagcgaggt 1020

acccattgcc actcccgatc aggctaaagg cttgccattg ttcctgcatg gctaagtgcc 1080

tgggtttgtc ctaatagaac tgaacactgg tcactgggtt ccatggttct cttccatgac 1140

ccacggcttc taatagagct ataacactca ccgcatggcc caagattcca ttccttggta 1200

tctgtgaggc caagaacccc aggtcagaga angtgaggct tgccaccatt tgggaagtgg 1260

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<212> PRT

<213> MSRV

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<220>

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<222> (46)..(46)

<223> Xaa = any amino acid

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Cys Leu Phe Leu Gly Glu Glu Cys Cys Xaa Tyr Val Asn Gln Ser Gly
20 25 30

Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg
35 40 45

Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp
50 55 60

Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe
65 70 75 80

Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val
85 90 95

Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu
100 105 110

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg
115 120 125

Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro
130 135 140

Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly
145 150 155 160

Ser Ser

<210> 14

<211> 21

<212> DNA

<213> MSRV

<400> 14

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<210> 15

<211> 21

<212> DNA

<213> MSRV

<400> 15

catgtcacca gggtggaata g 21

<210> 16

<211> 758

<212> DNA

<213> MSRV

<400> 16

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atgttccttc aggagaacaa agaacaggcc attacccagg ggaagactgg caactagatt 180

ttacccacat ggccaaatgt cagggatttc agcatctact agtctgggca gatactttca 240

ctggttgggt ggagtcttct ccttgtagga cagaaaagac ccaagaggta ataaaggcac 300

taatgaaata attcccagat ttggacttcc cccaggatta cagggtgaca atggccccgc 360

tttcaaggct gcagtaaccc agggagtatc ccaggtgtta ggcatacaat atcacttaca 420

ctgtgcctgg aggccacaat cctccagaaa agtcaagaaa atgaatgaaa cactcaaaga 480

tctaaaaaag ctaacccaag aaacccacat tgcatgacct gttctgttgc ctataacctt 540

actaagaatc cataactatc ccccaaaaag caggacttag cccatacgag atgctatatg 600

gatggccttt cctaaccaat gaccttgtgc ttgactgaga aatggccaac ttagttgcag 660

acatcacctc cttagccaaa tatcaacaag ttcttaaaac atcacaggga acctgtcccc 720

gagaggaggg aaaggaacta ttccaccctg gtgacatg 758

<210> 17

<211> 25

<212> DNA

<213> MSRV

<400> 17
cggacatcca aagtgatggg aaacg 25

<210> 18

<211> 26

<212> DNA

<213> MSRV

<400> 18
ggacaggaaa gtaagactga gaaggc 26

<210> 19

<211> 26

<212> DNA

<213> MSRV

<400> 19
cctagaacgt attctggaga attggg 26

<210> 20

<211> 26

<212> DNA

<213> MSRV

<400> 20

tggctctcaa tggtcaaaca tacccg 26

<210> 21

<211> 1511

<212> DNA

<213> MSRV

<400> 21

cctagaacgt attctggaga attgggacca atgtgacact cagacgctaa gaaagaaacg 60

atttatattc ttctgcagta ccgcctggcc acaatatcct cttcaaggga gagaaacctg 120

gcttcctgag ggaagtataa attataacat catcttacag ctagacctct tctgtagaaa 180

ggagggcaaa tggagtgaag tgccatatgt gcaaactttc ttttcattaa gagacaactc 240

acaattatgt aaaaagtgtg gtttatgccc tacaggaagc cctcagagtc cacctcccta 300

ccccagcgtc ccctccccga ctccttcctc aactaataag gacccccctt taacccaaac 360

ggtccaaaag gagatagaca aaggggtaaa caatgaacca aagagtgcca atattccccg 420

attatgcccc ctccaagcag tgagaggagg agaattcggc ccagccagag tgcctgtacc 480

tttttctctc tcagacttaa agcaaattaa aatagaccta ggtaaattct cagataaccc 540

tgacggctat attgatgttt tacaagggtt aggacaatcc tttgatctga catggagaga 600

tataatgtta ctactaaatc agacactaac cccaaatgag agaagtgccg ctgtaactgc 660

agcccgagag tttggcgatc tttggtatct cagtcaggcc aacaatagga tgacaacaga 720

ggaaagaaca actcccacag gccagcaggc agttcccagt gtagaccctc attgggacac 780

agaatcagaa catggagatt ggtgccacaa acatttgcta acttgcgtgc tagaaggact 840

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ggaagaaaat cttactgctt ttctggacag actaagggag gcattgagga agcatacctc 960

cctgtcacct gactctattg aaggccaact aatcttaaag gataagttta tcactcagtc 1020

agctgcagac attagaaaaa acttcaaaag tctgccttag gcccggagca gaacttagaa 1080

accctattta acttggcatc ctcagttttt tataatagag atcaggagga gcaggcgaaa 1140

cgggacaaac gggataaaaa aaaaaggggg ggtccactac tttagtcatg gccctcaggc 1200

aagcagactt tggaggctct gcaaaaggga aaagctgggc aaatcaaatg cctaataggg 1260

ctggcttcca gtgcggtcta caaggacact ttaaaaaaga ttatccaagt agaaataagc 1320

cgccccttg tccatgcccc ttacgtcaag ggaatcactg gaaggcccac tgccccaggg 1380

gatgaagata ctctgagtca gaagccatta accagatgat ccagcagcag gactgagggt 1440

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<211> 352

<212> PRT

<213> MSRV

<400> 22

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1 5 10 15

Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr
20 25 30

Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr
35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp
50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser
65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser
85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn
100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly
115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu
130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro
145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe
165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln
180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr
195 200 205

Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe
210 215 220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu
225 230 235 240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro
245 250 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu
260 265 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met
275 280 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu
290 295 300

Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser
305 310 315 320

Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe
325 330 335

Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro
340 345 350

<210> 23

<211> 30

<212> DNA

<213> MSRV

<400> 23

tgctggaatt cgggatccta gaacgtattc 30

<210> 24

<211> 30

<212> DNA

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<400> 24

agttctgctc cgaagcttag gcagactttt 30

<210> 25

<211> 398

<212> PRT

<213> MSRV

<400> 25

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
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Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
20 25 30

Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr
35 40 45

Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln
50 55 60

Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn
65 70 75 80

Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys
85 90 95

Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn
100 105 110

Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln
115 120 125

Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr
130 135 140

Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys
145 150 155 160

Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro
165 170 175

Leu Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val
180 185 190

Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys
195 200 205

Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly
210 215 220

Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln
225 230 235 240

Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu
245 250 255

Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr
260 265 270

Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp
275 280 285

Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His
290 295 300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro
305 310 315 320

Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn
325 330 335

Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr
340 345 350

Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys
355 360 365

Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu
370 375 380

Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His
385 390 395

<210> 26

<211> 378

<212> PRT

<213> MSRV

<400> 26

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg
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20 25 30

Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln
35 40 45

Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile
50 55 60

Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val
65 70 75 80

Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys
85 90 95

Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro
100 105 110

Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro
115 120 125

Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn
130 135 140

Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val
145 150 155 160

Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu
165 170 175

Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn
180 185 190

Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp
195 200 205

Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro
210 215 220

Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu
225 230 235 240

Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr
245 250 255

Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp
260 265 270

Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys
275 280 285

Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser
290 295 300

Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe
305 310 315 320

Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro
325 330 335

Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln
340 345 350

Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala
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Ala Ala Leu Glu His His His His His His

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<212> DNA

<213> MSRV

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<210> 29

<211> 25

<212> DNA

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<212> DNA

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<400> 30

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tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180

ctgcatggtc caagattcca ttccttggaa tccgtgagac caagaacccc aggtcagaga 240

acacaaggct tgccaccatg ttggaagcag cccaccacca ttttggaagc agcccgccac 300

tatcttggga gctctgggag caaggacccc aggtaacaat ttggtgacca cgaagggacc 360

tgaatccgca accatgaagg gatctccaaa gcaattggaa atgttcctcc caaggcaaaa 420

atgcccctaa gatgtattct ggagaattgg gaccaatttg accctcagac agtaagaaaa 480

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aacctggcct cctgagggaa gtataaatta taacaccatc ttacagctag acctgttttg 600

tagaaaagga ggcaaatgga gtgaagtgcc atatttacaa actttctttt cattaaaaga 660

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<211> 800

<212> DNA

<213> MSRV

<400> 31

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tcactgggtt ccacggttct cttccatgac ccatggcttc taatagagct ataacactca 180

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<211> 65

<212> PRT

<213> MSRV

<400> 32

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20 25 30

Arg Leu Ala Thr Met Leu Glu Ala Ala His His His Phe Gly Ser Ser
35 40 45

Pro Pro Leu Ser Trp Glu Leu Trp Glu Gln Gly Pro Gln Val Thr Ile
50 55 60

Trp
65

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<211> 26

<212> DNA

<213> MSRV

<400> 33
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<210> 34

<211> 28

<212> DNA

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<400> 34

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<210> 35

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<400> 35

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<210> 36

<211> 31

<212> DNA

<213> MSRV

<400> 36

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<210> 37

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<400> 37

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<210> 38

<211> 33

<212> DNA

<213> MSRV

<400> 38

cggcagtagc agtcttagta tctgaagcag tta 33

<210> 39

<211> 28

<212> DNA

<213> MSRV

<400> 39

ggtacggagg gtttcatgta gttttgag 28

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<211> 1247

<212> DNA

<213> MSRV

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tgggaccaat gtgacactca gacgctaaga aagaaacgat ttatattctt ctgcagtacc 180

gcctggccac aatatcctct tcaagggaga gaaacctggc ttcctgaggg aagtataaat 240

tataacatca tcttacagct agacctcttc tgtagaaagg agggcaaatg gagtgaagtg 300

ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 360

ttatgcccta caggaagccc tcagagtcca cctccctacc ccagcgtccc ctccccgact 420

ccttcctcaa ctaataagga ccccccttta acccaaacgg tccaaaagga gatagacaaa 480

ggggtaaaca atgaaccaaa gagtgccaat attccccgat tatgcccccc ccaagcagtg 540

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caaattaaaa tagacctagg taaattctca gataaccctg acggctatat tgatgtttta 660

caagggttag gacaatcctt tgatctgaca tggagagata taatgttact actaaatcag 720

acactaaccc caaatgagag aagtgccgct gtaactgcag cccgagagtt tggcgatctt 780

tggtatctca gtcaggccaa caataggatg acaacagagg aaagaacaac tcccacaggc 840

cagcaggcag ttcccagtgt agaccctcat tgggacacag aatcagaaca tggagattgg 900

tgccacaaac atttgctaac ttgcgtgcta gaaggactga ggaaaactag gaagaagcct 960

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ggccaactaa tcttaaagga taagtttatc actcagtcag ctgcagacat tagaaaaaac 1140

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<210> 41

<211> 1186

<212> DNA

<213> MSRV

<400> 41

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gcctggccac aatatcctct tcaagggaga gaaacctggc ttcctgaggg aagtataaat 180

tataacatca tcttacagct agacctcttc tgtagaaagg agggcaaatg gagtgaagtg 240

ccatatgtgc aaactttctt ttcattaaga gacaactcac aattatgtaa aaagtgtggt 300

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<211> 2030

<212> DNA

<213> MSRV

<400> 42

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acgcggcttc ctggaaatat tgatgcccca tcatatagga gtttatctaa gggaaactcc 180

accttcactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg 240

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agcaatacta tagacacaac cagctcccaa tgcatcaggt gggtaacacc tcccacacga 780

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<210> 43

<211> 2055

<212> DNA

<213> MSRV

<400> 43

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agaaccccag gtcagagaac acaaggcttg ccaccatgtt ggaagcagcc caccaccatt 480

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actcagacgc taagaaagaa acgatttata ttcttctgca gtaccgcctg gccacaatat 720

cctcttcaag ggagagaaac ctggcttcct gagggaagta taaattataa catcatctta 780

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<211> 1197

<212> DNA

<213> MSRV

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cccctgcctt atcgccaagc tccttcagga gaacaaagaa caggcaatta cccaagagaa 360

gactggcaac tagattttat ccacatgcca aaatcacagg gatttcagtg tctactagtc 420

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cacactcgaa tcaaaccctg gatactgccg aaggaacccg aaaatccagg ggacaacgct 1140

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<211> 1718

<212> DNA

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gaaagaagta gtaaagaaaa aacagtatac cctattcctt taaaagccag ggtaaatttc 180

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